



SEQUENCE LISTING

<110> Skeiky, Yasir
Guderian, Jeffrey
Corixa Corporation

<120> Methods of Using a Mycobacterium tuberculosis Coding Sequence to Facilitate Stable and High Yield Expression of Heterologous Proteins

<130> 014058-008010US

<140> US 09/684,215

<141> 2000-10-06

<150> US 60/158,585

<151> 1999-10-07

<160> 23

<170> PatentIn Ver. 2.1

<210> 1

<211> 1872

<212> DNA

<213> Mycobacterium tuberculosis

<220>

<223> 32 KD serine protease MTB32A

<220>

<221> CDS

<222> (89)..(1156)

<223> MTB32A

<220>

<221> sig_peptide

<222> (89)..(184)

<223> N-terminal hydrophobic secretory signal sequence

<220>

<221> mat_peptide

<222> (185)..(1153)

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Met Ser Asn Ser Arg Arg Arg Ser
-30 -25

ctc agg tgg tca tgg ttg ctg agc gtg ctg gct gcc gtc ggg ctg ggc 160
Leu Arg Trp Ser Trp Leu Leu Ser Val Leu Ala Ala Val Gly Leu Gly
-20 -15 -10

ctg gcc acg gcg ccg gcc cag gcg gcc ccg ccg gcc ttg tcg cag gac 208
Leu Ala Thr Ala Pro Ala Gln Ala Ala Pro Pro Ala Leu Ser Gln Asp
-5 -1 1 5

ggc gca cga gtc caa cgc gtg gtc ggg agc gct ccg gcg gca agt ctc	976		
Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu			
250	255	260	
ggc atc tcc acc ggc gac gtg atc acc gcg gtc gac ggc gct ccg atc	1024		
Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile			
265	270	275	280
aac tcg gcc acc gcg atg gcg gac gcg ctt aac ggg cat cat ccc ggt	1072		
Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly			
285	290	295	
gac gtc atc tcg gtg acc tgg caa acc aag tcg ggc ggc acg cgt aca	1120		
Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr			
300	305	310	
ggg aac gtg aca ttg gcc gag gga ccc ccg gcc tga tttcgctcg	1166		
Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala			
315	320		
gataccaccc gccggccggc caattggatt ggccgcagcc gtgattgccg cgtgagcccc	1226		
cggatccgt ctcccggtcg cgtggcatcg tggaaagcaat gaacgaggca gaacacagcg	1286		
tgcggcaccc tcccgtgcag ggcagtacg tcgaaggcgg tgtggtcgag catccggatg	1346		
ccaaggactt cggcagcgcc gccgcctgc ccgcccgtcc gacctggttt aagcacgccc	1406		
tcttctacga ggtgctggtc cggcggttct tcgacgcccag cgccggacggt tccggcgatc	1466		
tgcgtggact catcgatcgc ctcgactacc tgcatgtggct tggcatcgac tgcacatctgg	1526		
tgcggccgtt ctacgactcg ccgctgcgcg acggcggtta cgacattcgc gacttctaca	1586		
aggtgctgcc cgaattcgcc accgtcgacg atttcgtcgc cctggtcgac gccgctcacc	1646		
ggcgaggtat ccgcacatc accgacctgg tgcacatca cacctcgag tgcacccct	1706		
ggtttcagga gtcccgccgc gacccagacg gaccgtacgg tgactattac gtgtggagcg	1766		
acaccagcga gcgctacacc gacgccccga tcatcttcgt cgacaccgaa gagtcgaact	1826		
ggtcattcga tcctgtccgc cgacagttct actggcacccg attctt	1872		

<210> 2
<211> 355
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> 32 KD serine protease MTB32A

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20	25	30				
Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala Leu						
35	40	45				

Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Gly Pro Gln Val Val
 50 55 60
 Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr
 65 70 75 80
 Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
 85 90 95
 Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
 100 105 110
 Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
 115 120 125
 Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
 130 135 140
 Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly
 145 150 155 160
 Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu
 165 170 175
 Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu Thr
 180 185 190
 Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser
 195 200 205
 Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr
 210 215 220
 Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gln Gly Phe Ala
 225 230 235 240
 Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser Gly
 245 250 255
 Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly Leu
 260 265 270
 Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val Val
 275 280 285
 Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val Ile
 290 295 300
 Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala Asp
 305 310 315 320
 Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Thr Trp Gln
 325 330 335
 Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu Gly
 340 345 350
 Pro Pro Ala
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<210> 3
 <211> 396
 <212> DNA
 <213> Mycobacterium tuberculosis

<220>
 <223> 14 KD C-terminal fragment of MTB32A Ra12

<220>
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 <222> (1)..(396)
 <223> Ra12

<400> 3
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gcc att ccg atc ggg cag gcg atg gcg atc gcg ggc cag atc cga tcg	96
Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser	
20	25
25	30
ggt ggg ggg tca ccc acc gtt cat atc ggg cct acc gcc ttc ctc ggc	144
Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly	
35	40
40	45
ttg ggt gtt gtc gac aac aac ggc aac ggc gca cga gtc caa cgc gtg	192
Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val	
50	55
55	60
gtc ggg agc gct ccg gcg gca agt ctc ggc atc tcc acc ggc gac gtg	240
Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val	
65	70
70	75
75	80
atc acc gcg gtc gac ggc gct ccg atc aac tcg gcc acc gcg atg gcg	288
Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala	
85	90
90	95
gac gcg ctt aac ggg cat cat ccc ggt gac gtc atc tcg gtg acc tgg	336
Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Thr Trp	
100	105
105	110
caa acc aag tcg ggc ggc acg cgt aca ggg aac gtg aca ttg gcc gag	384
Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu	
115	120
120	125
gga ccc ccg gcc	396
Gly Pro Pro Ala	
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<210> 4
<211> 132
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> 14 KD C-terminal fragment of MTB32A Ra12

<400> 4
Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
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Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser
20 25 30
Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
35 40 45
Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val
50 55 60
Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
65 70 75 80
Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
85 90 95
Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Thr Trp
100 105 110
Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
115 120 125
Gly Pro Pro Ala
130

<210> 5
 <211> 702
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ra12-DPPP fusion polypeptide

<220>
 <221> CDS
 <222> (4) .. (696)
 <223> Ra12-DPPP fusion polypeptide

<400> 5

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1 5 10 15	
ctg tcc cag ggt ggg cag gga ttc gcc att ccg atc ggg cag gcg atg	96
Leu Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met	
20 25 30	
gcg atc gcg ggc cag atc cga tcg ggt ggg tca ccc acc gtt cat	144
Ala Ile Ala Gly Gln Ile Arg Ser Gly Gly Ser Pro Thr Val His	
35 40 45	
atc ggg cct acc gcc ttc ctc ggc ttg ggt gtt gtc gac aac aac ggc	192
Ile Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly	
50 55 60	
aac ggc gca cga gtc caa cgc gtg gtc ggg agc gct ccg gcg gca agt	240
Asn Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser	
65 70 75	
ctc ggc atc tcc acc ggc gac gtg atc acc gcg gtc gac ggc gct ccg	288
Leu Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro	
80 85 90 95	
atc aac tcg gcc acc gcg atg gcg gac gcg ctt aac ggg cat cat ccc	336
Ile Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro	
100 105 110	
ggt gac gtc atc tcg gtg acc tgg caa acc aag tcg ggc ggc acg cgt	384
Gly Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg	
115 120 125	
aca ggg aac gtg aca ttg gcc gag gga ccc ccg gcc gaa ttc gac gac	432
Thr Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala Glu Phe Asp Asp	
130 135 140	
gac gac aag gat cca cct gac ccg cat cag ccg gac atg acg aaa ggc	480
Asp Asp Lys Asp Pro Pro Asp Pro His Gln Pro Asp Met Thr Lys Gly	
145 150 155	
tat tgc ccg ggt ggc cga tgg ggt ttt ggc gac ttg gcc gtg tgc gac	528
Tyr Cys Pro Gly Gly Arg Trp Gly Phe Gly Asp Leu Ala Val Cys Asp	
160 165 170 175	

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ggc gag aag tac ccc gac ggc tcg ttt tgg cac cag tgg atg caa acg 576
Gly Glu Lys Tyr Pro Asp Gly Ser Phe Trp His Gln Trp Met Gln Thr
180          185          190

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tgg ttt acc ggc cca cag ttt tac ttc gat tgt gtc agc ggc ggt gag 624
Trp Phe Thr Gly Pro Gln Phe Tyr Phe Asp Cys Val Ser Gly Gly Glu
195 200 205

ccc ctc ccc ggc ccg ccg cca ccg ggt ggt tgc ggt ggg gca att ccg 672
 Pro Leu Pro Gly Pro Pro Pro Pro Gly Gly Gly Cys Gly Gly Ala Ile Pro
 210 215 220

tcc gag cag ccc aac gct ccc tga gaattc 702
Ser Glu Gln Pro Asn Ala Pro
225 230

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<210> 6
<211> 230
<212> PRT
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence:Rat2-DPPD fusion
polypeptide

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<400> 6
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      20          25          30
Ile Ala Gly Gln Ile Arg Ser Gly Gly Ser Pro Thr Val His Ile
      35          40          45
Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn
      50          55          60
Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu
      65          70          75          80
Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile
      85          90          95
Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly
      100         105         110
Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr
      115         120         125
Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala Glu Phe Asp Asp Asp
      130         135         140
Asp Lys Asp Pro Pro Asp Pro His Gln Pro Asp Met Thr Lys Gly Tyr
      145         150         155         160
Cys Pro Gly Gly Arg Trp Gly Phe Gly Asp Leu Ala Val Cys Asp Gly
      165         170         175
Glu Lys Tyr Pro Asp Gly Ser Phe Trp His Gln Trp Met Gln Thr Trp
      180         185         190
Phe Thr Gly Pro Gln Phe Tyr Phe Asp Cys Val Ser Gly Gly Glu Pro
      195         200         205
Leu Pro Gly Pro Pro Pro Gly Gly Cys Gly Gly Ala Ile Pro Ser
      210         215         220
Glu Gln Pro Asn Ala Pro
      225         230

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<210> 7
<211> 1746
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Ra12-WT1 fusion

<220>
<221> CDS
<222> (4)..(1740)
<223> Ra12-WT1 fusion polypeptide

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    Met His His His His His Thr Ala Ala Ser Asp Asn Phe Gln
    1           5           10          15

ctg tcc cag ggt ggg cag gga ttc gcc att ccg atc ggg cag gcg atg      96
Leu Ser Gln Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met
    20          25          30

gcg atc gcg ggc cag atc cga tcg ggt ggg ggg tca ccc acc gtt cat     144
Ala Ile Ala Gly Gln Ile Arg Ser Gly Gly Ser Pro Thr Val His
    35          40          45

atc ggg cct acc gcc ttc ctc ggc ttg ggt gtt gtc gac aac aac ggc     192
Ile Gly Pro Thr Ala Phe Leu Gly Leu Val Val Asp Asn Asn Gly
    50          55          60

aac ggc gca cga gtc caa cgc gtg gtc ggg agc gct ccg gcg gca agt     240
Asn Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser
    65          70          75

ctc ggc atc tcc acc ggc gac gtg atc acc gcg gtc gac ggc gct ccg     288
Leu Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro
    80          85          90          95

atc aac tcg gcc acc gcg atg gcg gac gcg ctt aac ggg cat cat ccc     336
Ile Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro
    100         105         110

ggg gac gtc atc tcg gtg acc tgg caa acc aag tcg ggc ggc acg cgt     384
Gly Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg
    115         120         125

aca ggg aac gtg aca ttg gcc gag gga ccc ccg gcc gaa ttc ccg ctg     432
Thr Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala Glu Phe Pro Leu
    130         135         140

gtg ccg cgc ggc agc ccg atg ggc tcc gac gtt cggt gac ctg aac gca     480
Val Pro Arg Gly Ser Pro Met Gly Ser Asp Val Arg Asp Leu Asn Ala
    145         150         155

ctg ctg ccg gca gtt ccg tcc ctg ggt ggt ggt ggt tgc gca ctg      528
Leu Leu Pro Ala Val Pro Ser Leu Gly Gly Gly Gly Cys Ala Leu
    160         165         170         175

ccg gtt agc ggt gca gca cag tgg gct ccg gtt ctg gac ttc gca ccg     576
Pro Val Ser Gly Ala Ala Gln Trp Ala Pro Val Leu Asp Phe Ala Pro
    180         185         190

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ccg ggt gca tcc gca tac ggt tcc ctg ggt ggt ccg gca ccg ccg ccg Pro Gly Ala Ser Ala Tyr Gly Ser Leu Gly Gly Pro Ala Pro Pro Pro 195 200 205	624
gca ccg ccg ccg ccg ccg ccg ccg cac tcc ttc atc aaa cag Ala Pro Pro Pro Pro Pro Pro His Ser Phe Ile Lys Gln 210 215 220	672
gaa ccg agc tgg ggt ggt gca gaa ccg cac gaa gaa cag tgc ctg agc Glu Pro Ser Trp Gly Gly Ala Glu Pro His Glu Glu Gln Cys Leu Ser 225 230 235	720
gca ttc acc gtt cac ttc tcc ggc cag ttc act ggc aca gcc gga gcc Ala Phe Thr Val His Phe Ser Gly Gln Phe Thr Gly Thr Ala Gly Ala 240 245 250 255	768
tgt cgc tac ggg ccc ttc ggt cct cct ccg ccc agc cag gcg tca tcc Cys Arg Tyr Gly Pro Phe Gly Pro Pro Ser Gln Ala Ser Ser 260 265 270	816
ggc cag gcc agg atg ttt cct aac gcg ccc tac ctg ccc agc tgc ctc Gly Gln Ala Arg Met Phe Pro Asn Ala Pro Tyr Leu Pro Ser Cys Leu 275 280 285	864
gag agc cag ccc gct att cgc aat cag ggt tac agc acg gtc acc ttc Glu Ser Gln Pro Ala Ile Arg Asn Gln Gly Tyr Ser Thr Val Thr Phe 290 295 300	912
gac ggg acg ccc agc tac ggt cac acg ccc tcg cac cat gcg gcg cag Asp Gly Thr Pro Ser Tyr Gly His Thr Pro Ser His His Ala Ala Gln 305 310 315	960
ttc ccc aac cac tca ttc aag cat gag gat ccc atg ggc cag cag ggc Phe Pro Asn His Ser Phe Lys His Glu Asp Pro Met Gly Gln Gln Gly 320 325 330 335	1008
tcg ctg ggt gag cag tac tcg gtg ccg ccc ccg gtc tat ggc tgc Ser Leu Gly Glu Gln Gln Tyr Ser Val Pro Pro Val Tyr Gly Cys 340 345 350	1056
cac acc ccc acc gac agc tgc acc ggc agc cag gct ttg ctg ctg agg His Thr Pro Thr Asp Ser Cys Thr Gly Ser Gln Ala Leu Leu Leu Arg 355 360 365	1104
acg ccc tac agc agt gac aat tta tac caa atg aca tcc cag ctt gaa Thr Pro Tyr Ser Ser Asp Asn Leu Tyr Gln Met Thr Ser Gln Leu Glu 370 375 380	1152
tgc atg acc tgg aat cag atg aac tta gga gcc acc tta aag ggc cac Cys Met Thr Trp Asn Gln Met Asn Leu Gly Ala Thr Leu Lys Gly His 385 390 395	1200
agc aca ggg tac gag agc gat aac cac aca acg ccc atc ctc tgc gga Ser Thr Gly Tyr Glu Ser Asp Asn His Thr Thr Pro Ile Leu Cys Gly 400 405 410 415	1248
gcc caa tac aga ata cac acg cac ggt gtc ttc aga ggc att cag gat Ala Gln Tyr Arg Ile His Thr His Gly Val Phe Arg Gly Ile Gln Asp 420 425 430	1296

gtg cga cgt gtg cct gga gta gcc ccg act ctt gta cg ^g tcg gca tct Val Arg Arg Val Pro Gly Val Ala Pro Thr Leu Val Arg Ser Ala Ser	435	440	445	1344
gag acc agt gag aaa cgc ccc ttc atg tgt gct tac tca ggc tgc aat Glu Thr Ser Glu Lys Arg Pro Phe Met Cys Ala Tyr Ser Gly Cys Asn	450	455	460	1392
aag aga tat ttt aag ctg tcc cac tta cag atg cac agc agg aag cac Lys Arg Tyr Phe Lys Leu Ser His Leu Gln Met His Ser Arg Lys His	465	470	475	1440
act ggt gag aaa cca tac cag tgt gac ttc aag gac tgt gaa cga agg Thr Gly Glu Lys Pro Tyr Gln Cys Asp Phe Lys Asp Cys Glu Arg Arg	480	485	490	1488
ttt ttt cgt tca gac cag ctc aaa aga cac caa agg aga cat aca ggt Phe Phe Arg Ser Asp Gln Leu Lys Arg His Gln Arg Arg His Thr Gly	500	505	510	1536
gtg aaa cca ttc cag tgt aaa act tgt cag cga aag ttc tcc cg ^g tcc Val Lys Pro Phe Gln Cys Lys Thr Cys Gln Arg Lys Phe Ser Arg Ser	515	520	525	1584
gac cac ctg aag acc cac acc agg act cat aca ggt gaa aag ccc ttc Asp His Leu Lys Thr His Thr Arg Thr His Thr Gly Glu Lys Pro Phe	530	535	540	1632
agc tgt cg ^g tgg cca agt tgt cag aaa aag ttt gcc cg ^g tca gat gaa Ser Cys Arg Trp Pro Ser Cys Gln Lys Lys Phe Ala Arg Ser Asp Glu	545	550	555	1680
tta gtc cgc cat cac aac atg cat cag aga aac atg acc aaa ctc cag Leu Val Arg His His Asn Met His Gln Arg Asn Met Thr Lys Leu Gln	560	565	570	1728
ctg gcg ctt tga gaattc Leu Ala Leu				1746

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<210> 8
<211> 578
<212> PRT
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence:Ra12-WT1 fusion
polypeptide

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<400> 8
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      1           5           10          15
Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
      20          25          30
Ile Ala Gly Gln Ile Arg Ser Gly Gly Gly Ser Pro Thr Val His Ile
      35          40          45
Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn
      50          55          60
Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu
      65          70          75          80

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Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile
 85 90 95
 Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly
 100 105 110
 Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr
 115 120 125
 Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala Glu Phe Pro Leu Val
 130 135 140
 Pro Arg Gly Ser Pro Met Gly Ser Asp Val Arg Asp Leu Asn Ala Leu
 145 150 155 160
 Leu Pro Ala Val Pro Ser Leu Gly Gly Gly Cys Ala Leu Pro
 165 170 175
 Val Ser Gly Ala Ala Gln Trp Ala Pro Val Leu Asp Phe Ala Pro Pro
 180 185 190
 Gly Ala Ser Ala Tyr Gly Ser Leu Gly Gly Pro Ala Pro Pro Pro Ala
 195 200 205
 Pro Pro Pro Pro Pro Pro Pro His Ser Phe Ile Lys Gln Glu
 210 215 220
 Pro Ser Trp Gly Gly Ala Glu Pro His Glu Glu Gln Cys Leu Ser Ala
 225 230 235 240
 Phe Thr Val His Phe Ser Gly Gln Phe Thr Gly Thr Ala Gly Ala Cys
 245 250 255
 Arg Tyr Gly Pro Phe Gly Pro Pro Pro Ser Gln Ala Ser Ser Gly
 260 265 270
 Gln Ala Arg Met Phe Pro Asn Ala Pro Tyr Leu Pro Ser Cys Leu Glu
 275 280 285
 Ser Gln Pro Ala Ile Arg Asn Gln Gly Tyr Ser Thr Val Thr Phe Asp
 290 295 300
 Gly Thr Pro Ser Tyr Gly His Thr Pro Ser His His Ala Ala Gln Phe
 305 310 315 320
 Pro Asn His Ser Phe Lys His Glu Asp Pro Met Gly Gln Gln Gly Ser
 325 330 335
 Leu Gly Glu Gln Gln Tyr Ser Val Pro Pro Val Tyr Gly Cys His
 340 345 350
 Thr Pro Thr Asp Ser Cys Thr Gly Ser Gln Ala Leu Leu Leu Arg Thr
 355 360 365
 Pro Tyr Ser Ser Asp Asn Leu Tyr Gln Met Thr Ser Gln Leu Glu Cys
 370 375 380
 Met Thr Trp Asn Gln Met Asn Leu Gly Ala Thr Leu Lys Gly His Ser
 385 390 395 400
 Thr Gly Tyr Glu Ser Asp Asn His Thr Thr Pro Ile Leu Cys Gly Ala
 405 410 415
 Gln Tyr Arg Ile His Thr His Gly Val Phe Arg Gly Ile Gln Asp Val
 420 425 430
 Arg Arg Val Pro Gly Val Ala Pro Thr Leu Val Arg Ser Ala Ser Glu
 435 440 445
 Thr Ser Glu Lys Arg Pro Phe Met Cys Ala Tyr Ser Gly Cys Asn Lys
 450 455 460
 Arg Tyr Phe Lys Leu Ser His Leu Gln Met His Ser Arg Lys His Thr
 465 470 475 480
 Gly Glu Lys Pro Tyr Gln Cys Asp Phe Lys Asp Cys Glu Arg Arg Phe
 485 490 495
 Phe Arg Ser Asp Gln Leu Lys Arg His Gln Arg Arg His Thr Gly Val
 500 505 510
 Lys Pro Phe Gln Cys Lys Thr Cys Gln Arg Lys Phe Ser Arg Ser Asp
 515 520 525
 His Leu Lys Thr His Thr Arg Thr His Thr Gly Glu Lys Pro Phe Ser
 530 535 540
 Cys Arg Trp Pro Ser Cys Gln Lys Lys Phe Ala Arg Ser Asp Glu Leu
 545 550 555 560

Val Arg His His Asn Met His Gln Arg Asn Met Thr Lys Leu Gln Leu
565 570 575
Ala Leu

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<210> 9
<211> 672
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence:Ra12-human mammaglobin fusion

<220>
<221> CDS
<222> (4)..(666)
<223> Ra12-human gammaglobin fusion polypeptide

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<400> 9
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           1          5          10          15

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ctg tcc cag ggt ggg cag gga ttc gcc att ccg atc ggg cag gcg atg 96
 Leu Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met
 20 25 30

gcg atc gcg ggc cag atc cga tcg ggt ggg ggg tca ccc acc gtt cat 144
 Ala Ile Ala Gly Gln Ile Arg Ser Gly Gly Gly Ser Pro Thr Val His
 35 40 45

atc ggg cct acc gcc ttc ctc ggc ttg ggt gtt gtc gac aac aac ggc 192
Ile Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly
50 55 60

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aac ggc gca cga gtc caa cgc gtg gtc ggg agc gct ccg gcg gca agt 240
Asn Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser
          65           70           75

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ctc ggc atc tcc acc ggc gac gtg atc acc gcg gtc gac ggc gct ccg 288
 Leu Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro
 80 85 90 95

atc aac tcg gcc acc gcg atg gcg gac gcg ctt aac ggg cat cat cat ccc 336
Ile Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro
100 105 110

```

ggt gac gtc atc tcg gtg acc tgg caa acc aag tcg ggc ggc acg cgt 384
Gly Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg
          115           120           125

```

aca ggg aac gtg aca ttg gcc gag gga ccc ccg gcc gaa ttc atc gag 432
 Thr Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala Glu Phe Ile Glu
 130 135 140

gga agg ggc tct ggc tgc ccc tta ttg gag aat gtg att tcc aag aca 480
 Gly Arg Gly Ser Gly Cys Pro Leu Leu Glu Asn Val Ile Ser Lys Thr
 145 150 155

atc aat cca caa gtg tct aag act gaa tac aaa gaa ctt ctt caa gag	528
Ile Asn Pro Gln Val Ser Lys Thr Glu Tyr Lys Glu Leu Leu Gln Glu	
160 165 170 175	

```

ttc ata gac gac aat gcc act aca aat gcc ata gat gaa ttg aag gaa 576
Phe Ile Asp Asp Asn Ala Thr Thr Asn Ala Ile Asp Glu Leu Lys Glu
                    180          185          190

```

```

tgt ttt ctt aac caa acg gat gaa act ctg agc aat gtt gag gtg ttt 624
Cys Phe Leu Asn Gln Thr Asp Glu Thr Leu Ser Asn Val Glu Val Phe
                     195          200          205

```

```

atg caa tta ata tat gac agc agt ctt tgt gat tta ttt taa gaattc      672
Met Gln Leu Ile Tyr Asp Ser Ser Leu Cys Asp Leu Phe
          210           215           220

```

```
<210> 10
<211> 220
<212> PRT
<213> Artificial Sequence
```

<220>
<223> Description of Artificial Sequence:Ra12-human mammaglobin
fusion polypeptide

```

<400> 10
Met His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu
      1           5           10          15
Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
      20          25          30
Ile Ala Gly Gln Ile Arg Ser Gly Gly Ser Pro Thr Val His Ile
      35          40          45
Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn
      50          55          60
Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu
      65          70          75          80
Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile
      85          90          95
Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly
      100         105         110
Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr
      115         120         125
Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala Glu Phe Ile Glu Gly
      130         135         140
Arg Gly Ser Gly Cys Pro Leu Leu Glu Asn Val Ile Ser Lys Thr Ile
      145         150         155         160
Asn Pro Gln Val Ser Lys Thr Glu Tyr Lys Glu Leu Leu Gln Glu Phe
      165         170         175
Ile Asp Asp Asn Ala Thr Thr Asn Ala Ile Asp Glu Leu Lys Glu Cys
      180         185         190
Phe Leu Asn Gln Thr Asp Glu Thr Leu Ser Asn Val Glu Val Phe Met
      195         200         205
Gln Leu Ile Tyr Asp Ser Ser Leu Cys Asp Leu Phe
      210         215         220

```

```
<210> 11
<211> 2191
<212> DNA
<213> Artificial Sequence
```

<220>
<223> Description of Artificial Sequence: Ra12-H9-32A fusion
(Ra12-MTB39-MTB32A(N-ter) fusion)

<220>
<221> CDS
<222> (1)..(2190)
<223> Ra12-H9-32A (Ra12-MTB39-MTB32A(N-ter)) fusion polypeptide

<400> 11
atg cat cac cat cac cat cac acg gcc gcg tcc gat aac ttc cag ctg 48
Met His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu
1 5 10 15
tcc cag ggt ggg cag gga ttc gcc att ccg atc ggg cag gcg atg gcg 96
Ser Gln Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
20 25 30
atc gcg ggc cag atc cga tcg ggt ggg ggg tca ccc acc gtt cat atc 144
Ile Ala Gly Gln Ile Arg Ser Gly Gly Ser Pro Thr Val His Ile
35 40 45
ggg cct acc gcc ttc ctc ggc ttg ggt gtt gtc gac aac aac ggc aac 192
Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn
50 55 60
ggc gca cga gtc caa cgc gtg gtc ggg agc gct ccg gcg gca agt ctc 240
Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu
65 70 75 80
ggc atc tcc acc ggc gac gtg atc acc gcg gtc gac ggc gct ccg atc 288
Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile
85 90 95
aac tcg gcc acc gcg atg gcg gac gcg ctt aac ggg cat cat ccc ggt 336
Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly
100 105 110
gac gtc atc tcg gtg acc tgg caa acc aag tcg ggc ggc acg cgt aca 384
Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr
115 120 125
ggg aac gtg aca ttg gcc gag gga ccc ccg gcc gaa ttc atg gtg gat 432
Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala Glu Phe Met Val Asp
130 135 140
ttc ggg gcg tta cca ccg gag atc aac tcc gcg agg atg tac gcc ggc 480
Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly
145 150 155 160
ccg ggt tcg gcc tcg ctg gtg gcc gcg gct cag atg tgg gac agc gtg 528
Pro Gly Ser Ala Ser Leu Val Ala Ala Gln Met Trp Asp Ser Val
165 170 175
gcg agt gac ctg ttt tcg gcc gcg tcg gcg ttt cag tcg gtg gtc tgg 576
Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp
180 185 190
ggt ctg acg gtg ggg tcg tgg ata ggt tcg tcg gcg ggt ctg atg gtg 624
Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly Leu Met Val
195 200 205

aac ttg ggt cgg gcg gcc tcg gtc ggt tcg ttg tcg gtg ccg cag gcc Asn Leu Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val Pro Gln Ala 450 455 460	1392
tgg gcc gcg gcc aac cag gca gtc acc ccg gcg gcg ccg gcg ctg ccg Trp Ala Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg Ala Leu Pro 465 470 475 480	1440
ctg acc agc ctg acc agc gcc gcg gaa aga ggg ccc ggg cag atg ctg Leu Thr Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly Gln Met Leu 485 490 495	1488
ggc ggg ctg ccg gtg ggg cag atg ggc gcc agg gcc ggt ggt ggg ctc Gly Gly Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly Gly Gly Leu 500 505 510	1536
agt ggt gtg ctg cgt gtt ccg ccg cga ccc tat gtg atg ccg cat tct Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met Pro His Ser 515 520 525	1584
ccg gca gcc ggc gat atc gcc ccg ccg gcc ttg tcg cag gac cgg ttc Pro Ala Ala Gly Asp Ile Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe 530 535 540	1632
gcc gac ttc ccc gcg ctg ccc ctc gac ccg tcc gcg atg gtc gcc caa Ala Asp Phe Pro Ala Leu Pro Leu Asp Pro Ser Ala Met Val Ala Gln 545 550 555 560	1680
gtg ggg cca cag gtg gtc aac atc aac acc aaa ctg ggc tac aac aac Val Gly Pro Gln Val Val Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn 565 570 575	1728
gcc gtg ggc gcc ggg acc ggc atc gtc atc gat ccc aac ggt gtc gtg Ala Val Gly Ala Gly Thr Gly Ile Val Ile Asp Pro Asn Gly Val Val 580 585 590	1776
ctg acc aac aac cac gtg atc gcg ggc gcc acc gac atc aat gcg ttc Leu Thr Asn Asn His Val Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe 595 600 605	1824
agc gtc ggc tcc ggc caa acc tac ggc gtc gat gtg gtc ggg tat gac Ser Val Gly Ser Gly Gln Thr Tyr Gly Val Asp Val Val Gly Tyr Asp 610 615 620	1872
cgc acc cag gat gtc gcg gtg ctg cag ctg cgc ggt gcc ggt ggc ctg Arg Thr Gln Asp Val Ala Val Leu Gln Leu Arg Gly Ala Gly Gly Leu 625 630 635 640	1920
ccg tcg gcg gcg atc ggt ggc ggc gtc gcg gtt ggt gag ccc gtc gtc Pro Ser Ala Ala Ile Gly Gly Val Ala Val Gly Glu Pro Val Val 645 650 655	1968
gcg atg ggc aac agc ggt ggg cag ggc gga acg ccc cgt gcg gtg cct Ala Met Gly Asn Ser Gly Gly Gln Gly Gly Thr Pro Arg Ala Val Pro 660 665 670	2016
ggc agg gtg gtc gcg ctc ggc caa acc gtg cag gcg tcg gat tcg ctg Gly Arg Val Val Ala Leu Gly Gln Thr Val Gln Ala Ser Asp Ser Leu 675 680 685	2064

acc ggt gcc gaa gag aca ttg aac ggg ttg atc cag ttc gat gcc gcg 2112
Thr Gly Ala Glu Glu Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala
690 695 700

atc cag ccc ggt gat tcg ggc ggg ccc gtc gtc aac ggc cta gga cag 2160
Ile Gln Pro Gly Asp Ser Gly Gly Pro Val Val Asn Gly Leu Gly Gln
705 710 715 720

gtg gtc ggt atg aac acg gcc gcg tcc tag g 2191
Val Val Gly Met Asn Thr Ala Ala Ser
725 730

<210> 12
<211> 729
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ra12-H9-32A fusion
polypeptide (Ra12-MTB39-MTB32A(N-ter) fusion polypeptide)

<400> 12
Met His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu
1 5 10 15
Ser Gln Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
20 25 30
Ile Ala Gly Gln Ile Arg Ser Gly Gly Ser Pro Thr Val His Ile
35 40 45
Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn
50 55 60
Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu
65 70 75 80
Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile
85 90 95
Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly
100 105 110
Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr
115 120 125
Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala Glu Phe Met Val Asp
130 135 140
Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly
145 150 155 160
Pro Gly Ser Ala Ser Leu Val Ala Ala Gln Met Trp Asp Ser Val
165 170 175
Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp
180 185 190
Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly Leu Met Val
195 200 205
Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr Ala Gly Gln
210 215 220
Ala Glu Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala Tyr Glu
225 230 235 240
Thr Ala Tyr Gly Leu Thr Val Pro Pro Val Ile Ala Glu Asn Arg
245 250 255
Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr
260 265 270
Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln
275 280 285
Asp Ala Ala Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr
290 295 300

Ala Thr Leu Leu Pro Phe Glu Glu Ala Pro Glu Met Thr Ser Ala Gly
 305 310 315 320
 Gly Leu Leu Glu Gln Ala Ala Ala Val Glu Glu Ala Ser Asp Thr Ala
 325 330 335
 Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu Gln Gln Leu
 340 345 350
 Ala Gln Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu
 355 360 365
 Trp Lys Thr Val Ser Pro His Arg Ser Pro Ile Ser Asn Met Val Ser
 370 375 380
 Met Ala Asn Asn His Met Ser Met Thr Asn Ser Gly Val Ser Met Thr
 385 390 395 400
 Asn Thr Leu Ser Ser Met Leu Lys Gly Phe Ala Pro Ala Ala Ala
 405 410 415
 Gln Ala Val Gln Thr Ala Ala Gln Asn Gly Val Arg Ala Met Ser Ser
 420 425 430
 Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly Val Ala Ala
 435 440 445
 Asn Leu Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val Pro Gln Ala
 450 455 460
 Trp Ala Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg Ala Leu Pro
 465 470 475 480
 Leu Thr Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly Gln Met Leu
 485 490 495
 Gly Gly Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly Gly Leu
 500 505 510
 Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met Pro His Ser
 515 520 525
 Pro Ala Ala Gly Asp Ile Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe
 530 535 540
 Ala Asp Phe Pro Ala Leu Pro Leu Asp Pro Ser Ala Met Val Ala Gln
 545 550 555 560
 Val Gly Pro Gln Val Val Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn
 565 570 575
 Ala Val Gly Ala Gly Thr Gly Ile Val Ile Asp Pro Asn Gly Val Val
 580 585 590
 Leu Thr Asn Asn His Val Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe
 595 600 605
 Ser Val Gly Ser Gly Gln Thr Tyr Gly Val Asp Val Val Gly Tyr Asp
 610 615 620
 Arg Thr Gln Asp Val Ala Val Leu Gln Leu Arg Gly Ala Gly Gly Leu
 625 630 635 640
 Pro Ser Ala Ala Ile Gly Gly Val Ala Val Gly Glu Pro Val Val
 645 650 655
 Ala Met Gly Asn Ser Gly Gly Gln Gly Thr Pro Arg Ala Val Pro
 660 665 670
 Gly Arg Val Val Ala Leu Gly Gln Thr Val Gln Ala Ser Asp Ser Leu
 675 680 685
 Thr Gly Ala Glu Glu Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala
 690 695 700
 Ile Gln Pro Gly Asp Ser Gly Gly Pro Val Val Asn Gly Leu Gly Gln
 705 710 715 720
 Val Val Gly Met Asn Thr Ala Ala Ser
 725

<210> 13
 <211> 51
 <212> DNA
 <213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence:oligonucleotide
      primer for PCR amplification of Ra12 C-terminal
      fragment of MTB32A

<400> 13
caattacata tgcacatcacca tcaccatcac acggccgcgt ccgataactt c      51

<210> 14
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:3'
      oligonucleotide primer for PCR amplification of
      Ra12 C-terminal fragment of MTB32A

<400> 14
ctaattcgaat tcggccgggg gtccctcgac caa      33

<210> 15
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:5'
      oligonucleotide primer containing enterokinase
      recognition site for PCR amplification of DPPD
      mature secreted form

<400> 15
caattagaat tcgacgacga cgacaaggat ccacactgacc cgcattcag      48

<210> 16
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:3'
      oligonucleotide primer containing enterokinase
      recognition site for PCR amplification of DPPD
      mature secreted form

<400> 16
caattagaat tctcaggggag cgttgggctg ctc      33

<210> 17
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Ra12 (short)
      polypeptide

```

<400> 17
Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
1 5 10 15
Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile
20 25 30

<210> 18
<211> 128
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Ra12(long)
polypeptide

<400> 18
Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
1 5 10 15
Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Lys Leu
20 25 30
Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val
35 40 45
Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala
50 55 60
Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val
65 70 75 80
Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn
85 90 95
Gly His His Pro Gly Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser
100 105 110
Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala
115 120 125

<210> 19
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:5'
oligonucleotide primer, HindIII site, for PCR
amplification of human gammaglobin

<400> 19
gcgaagctta tgaagttgct gatggtcctc atgc

34

<210> 20
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:3'
oligonucleotide primer, XbaI site, for PCR
amplification of human gammaglobin

<400> 20
cggctcgagt taaaataaat cacaaggact gctgtc

36

```

<210> 21
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Met-His tag 6aa

<400> 21
Met His His His His His His
    1           5

<210> 22
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:enterokinase
      recognition site

<400> 22
Asp Asp Asp Lys
    1

<210> 23
<211> 128
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> positions 1-128 of Ra12

<400> 23
Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
    1           5           10          15
Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser
    20          25          30
Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
    35          40          45
Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val
    50          55          60
Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
    65          70          75          80
Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
    85          90          95
Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Thr Trp
    100         105         110
Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
    115         120         125

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